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humanVR1 gene with translation of open reading frame

Input file Fchrb87a6.seq; Output File Fchrb87a6.tra
Sequence length 3909

GTGAGCGCAACGCACTGCGGGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGCAA
CGCACTGCGGGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCG
GCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGC
GCAACGCAGTGCGGGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTG
GCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTG
AGCGAACGCAGTGCGGGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTGAGCGAACGCAGTG
ACGCCAACGCTAATACGACTCACTATAGGAAAGCTGGTACGCCCTGCAGGTACCGGTCCCGAATTCCCGGGTCGACCC
ACCGCTCCGAAAACACACCTCTGCTGTGGAAAGACTGTGCAATGGCACAGCCGAGAGCTGGTTGGAGGTTGAA
GTGCTCTGGGGAGAATTCTGTAGATCATCCTCAGAAAAGCCTGCCCTGGTGTCTACCAAGAAAACGTCTCCCAATCAC
CCAGAAAAGCTGCCACAGTAGTCCCCCTTATCCACGGGTGTCACTTCCATGGTTCAAGTTATTCGCGGTCAACCAC
GGTCTGCCAATATTAATGGAAAATTCTCAAACAGTTCCAAGTTCCCTGTGATTGTTCTGAGCAGTGTGATGA
AGAGTCTCTGCCGTGCCATCTGGATGCAAACCGTCCCTGTGCCCCACGTCCAGGCCGTAGATGCTCCCCGCCGTC
AGTCACTTAGTCGTAGATGCCGTCTGGTATCACAGTGCTCTGTTCAAGGTTGCACACTGGGCCACAGAGGATCCA

M K K W S S T D L G T A A D P L Q K 18
GCAAGG ATG AAG AAA TGG AGC AGC ACA GAC TTG GGG ACA GCT GCG GAC CCA CTC CAA AAG 54

D T C P D P L D G D P N S R P P P A K P 38
GAC ACC TGC CCA GAC CCC CTG GAT GGA GAC CCT AAC TCC AGG CCA CCT CCA GCC AAG CCC 114

Q L P T A K S R T R L F G K G D S E E A 58
CAG CTC CCC ACG GCC AAG AGC CGC ACC CGG CTC TTT GGG AAG GGT GAC TCG GAG GAG GCT 174

F P V D C P H E E G E L D S C P T I T V 78
TTC CCG GTG GAT TGC CCC CAC GAG GAA GGT GAG TTG GAC TCC TGC CCG ACC ATC ACA GTC 234

S P V I T I Q R P G D G P T G A R L L S 98
AGC CCT GTT ATC ACC ATC CAG AGG CCA GGA GAC GGC CCC ACC GGT GCC AGG CTG CTG TCC 294

Fig. 1A

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Q D S V A A S T E K T L R L Y D R R S I 118
CAG GAC TCT GTC GCC GCC AGC ACC GAG AAG ACC CTC AGG CTC TAT GAT CGC AGG AGT ATC 354

F E A V A Q N N C Q D L E S L L L F L Q 138
TTT GAA GCC GTT GCT CAG AAT AAC TGC CAG GAT CTG GAG AGC CTG CTG CTC TTC CTG CAG 414

K S K K H L T D N E F K D P E T G K T C 158
AAG AGC AAG AAG CAC CTC ACA GAC AAC GAG TTC AAA GAC CCT GAG ACA GGG AAG ACC TGT 474

L L K A M L N L H D G Q N T T I P L L L 178
CTG CTG AAA GCC ATG CTC AAC CTG CAC GAC GGA CAG AAC ACC ACC ATC CCC CTG CTC CTG 534

E I A R Q T D S L K E L V N A S Y T D S 198
GAG ATC GCG CGG CAA ACG GAC AGC CTG AAG GAG CTT GTC AAC GCC AGC TAC ACG GAC AGC 594

Y Y K G Q T A L H I A I E R R N M A L V 218
TAC TAC AAG GGC CAG ACA GCA CTG CAC ATC GAC ATC GAG AGA CGC AAC ATG GCC CTG GTG 654

T L L V E N G A D V Q A A A A H G D F F K 238
ACC CTC CTG GTG GAG AAC GGA GCA GAC GTC CAG GCT GCG GCC CAT GGG GAC TTC TTT AAG 714

K T K G R P G F Y F G E L P L S L A A C 258
AAA ACC AAA GGG CGG CCT GGA TTC TAC TTC GGT GAA CTG CCC CTG TCC CTG GCC GCG TGC 774

T N Q L G I V K F L L Q N S W Q T A D I 278
ACC AAC CAG CTG GGC ATC GTG AAG TTC CTG CTG CAG AAC TCC TGG CAG ACG GCC GAC ATC 834

S A R D S V G N T V L H A L V E V A D N 298
AGC GCC AGG GAC TCG GTG GGC AAC ACG GTG CTG CAC GCC CTG GTG GAG GTG GCC GAC AAC 894

T A D N T K F V T S M Y N E I L M L G A 318
ACG GCC GAC AAC ACG AAG TTT GTG ACG AGC ATG TAC AAT GAG ATT CTG ATG CTG GGG GCC 954

K L H P T L K L E E L T N K K G M T P L 338
AAA CTG CAC CCG ACG CTG AAG CTG GAG GAC ACC AAC AAG GGA ATG ACG CCG CTG 1014

A L A A G T G K I G V L A Y I L Q R E I 358
GCT CTG GCA GCT GGG ACC GGG AAG ATC GGG GTC TTG GCC TAT ATT CTC CAG CGG GAG ATC 1074

Q E P E C R H L S R K F T E W A Y G P V 378
CAG GAG CCC GAG TGC AGG CAC CTG TCC AGG AAG TTC ACC GAG TGG GCC TAC GGG CCC GTG 1134

H S S L Y D L S C I D T C E K N S V L E 398
CAC TCC TCG CTG TAC GAC CTG TCC GAC ACC TGC GAG AAG AAC TCG GTG CTG GAG 1194

V I A Y S S S E T P N R H D M L L V E P 418
GTG ATC GCC TAC AGC AGC GAG ACC CCT AAT CGC CAC GAC ATG CTC TTG GTG GAG CCG 1254

Fig. 1B

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L N R L L Q D K W D R F V K R I F Y F N 438
CTG AAC CGA CTC CTG CAG GAC AAG TGG GAC AGA TTC GTC AAG CGC ATC TTC TAC TTC AAC 1314

F L V Y C L Y M I I F T M A A Y Y R P V 458
TTC CTG GTC TAC TGC CTG TAC ATG ATC ATC TTC ACC ATG GCT GCC TAC TAC AGG CCC GTG 1374

D G L P P F K M E K I G D Y F R V T G E 478
GAT GGC TTG CCT CCC TTT AAG ATG GAA ARA ATT GGA GAC TAT TTC CGA GTT ACT GGA GAG 1434

I L S V L G G V Y F F R G I Q Y F L Q 498
ATC CTG TCT GTG TTA GGA GGA GTC TAC TTC TTT TTC CGA GGG ATT CAG TAT TTC CTG CAG 1494

R R P S M K T L F V D S Y S E M L F F L 518
AGG CGG CCG TCG ATG AAG ACC CTG TTT GTG GAC AGC TAC AGT GAG ATG CTT TTC TTT CTG 1554

Q S L F M L A T V V L Y F S H L K E Y V 538
CAG TCA CTG TTC ATG CTG GCC ACC GTG GTG CTG TAC TTC AGC CAC CTC AAG GAG TAT GTG 1614

A S M V F S L A L G W T N M L Y Y T R G 558
GCT TCC ATG GTA TTC TCC CTG GCC TTG GGC TGG ACC AAC ATG CTC TAC TAC ACC CGC GGT 1674

F Q Q M G I Y A V M I E K M I L R D L C 578
TTC CAG CAG ATG GGC ATC TAT GCC GTC ATG ATA GAG AAG ATG ATC CTG AGA GAC CTG TGC 1734

R F M F V Y I V F L F G F S T A V V T L 598
CGT TTC ATG TTT GTC TAC ATC GTC TTC TTG TTC GGG TTT TCC ACA GCG GTG GTG ACG CTG 1794

I E D G K N D S L P S E S T S H R W R G 618
ATT GAA GAC GGG AAG AAT GAC TCC CTG CCG TCT GAG TCC ACG TCG CAC AGG TGG CGG GGG 1854

P A C R P P D S S Y N S L Y S T C L E L 638
CCT GCC TGC AGG CCC CCC GAT AGC TCC TAC AAC AGC CTG TAC TCC ACC TGC CTG GAG CTG 1914

F K F T I G M G D L E F T E N Y D F K A 658
TTC AAG TTC ACC ATC GGC ATG GGC GAC CTG GAG TTC ACT GAG AAC TAT GAC TTC AAG GCT 1974

V F I I L L A Y V I L T Y I L L L N M 678
GTC TTC ATC ATC CTG CTG GCC TAT GTA ATT CTC ACC TAC ATC CTC CTG CTC AAC ATG 2034

L I A L M G E T V N K I A Q E S K N I W 698
CTC ATC GCC CTC ATG GGT GAG ACT GTC AAC AAG ATC GCA CAG GAG AGC AAG AAC ATC TGG 2094

K L Q R A I T I L D T E K S F L K C M R 718
AAG CTG CAG AGA GCC ATC ACC ATC CTG GAC ACG GAG AAG AGC TTC CTT AAG TGC ATG AGG 2154

Fig. 1C

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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K A F R S G K L L Q V G Y T P D G K D D 738
AAG GCC TTC CGC TCA GGC AAG CTG CTG CAG GTG GGG TAC ACA CCT GAT GGC AAG GAC GAC 2214

Y R W C F R V D E V N W T T W N T N V G 758
TAC CGG TGG TGC TTC AGG GTG GAC GAG GTG AAC TGG ACC ACC TGG AAC ACC AAC GTG GGC 2274

I I N E D P G N C E G V K R T L S F S L 778
ATC ATC AAC GAA GAC CCG GGC AAC TGT GAG GGC GTC AAG CGC ACC CTG AGC TTC TCC CTG 2334

R S S R V S G R H W K N F A L V P L L R 798
CGG TCA AGC AGA GTT TCA GGC AGA CAC TGG AAG AAC TTT GCC CTG GTC CCC CTT TTA AGA 2394

E A S A R D R Q S A Q P E E V Y L R Q F 818
GAG GCA AGT GCT CGA GAT AGG CAG TCT GCT CAG CCC GAG GAA GTT TAT CTG CGA CAG TTT 2454

S G S L K P E D A E V F K S P A A S G E 838
TCA GGG TCT CTG AAG CCA GAG GAC GCT GAG GTC TTC AAG AGT CCT GCC GCT TCC GGG GAG 2514

K * 840
AAG TGA 2520

GGACGTCACGCAGACAGCACTGTCAACACTGGGCCTTAGGAGACCCCGTTGCCACGGGGGCTGCTGAGGGAACACCAAG
TGCTCTGTCAGCAGCCTGGCCTGGCTGTGCCTGCCAGCATGTTCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGT
TCTTGGAAGCATGGGAGTGATGTACATCCAACCGTCACTGTCCCCAAGTGAATCTCCTAACAGACTTCAAGGTTTTA
CTCACTTTACTAAAAAAAAAAAGGGCGGCCGTTA

Fig. 1D

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Full-length human VR2

Input file Flh21e11.seq; Output File Flh21e11.tra
 Sequence length 2809

GGCTAGCCTGTCTGACAGGGAGAGTTAACGCTCCGTTCTCCACCGTGCCGGCTGCCAGGTGGCTGAGGGTGACCG
 AGAGACCAGAACCTGCTTGAGCTTAGTGCTCAGAGCTGGGGAGGGAGGTTCCGCCCTCTGCTGTCAGCGCC
 GGCAGCCCCCTCCCGCTTCACTTCCTCCCGAGCCCCCTGCTACTGAGAAGCTCCGGATCCAGCAGCCGCCACGCCCT
 GGCCTCAGCCTGCAGGGCTCCAGTCAGGCCAACACCGACCGCAGCTGGGAGGAAGACAGGACCCCTGACATCTCCATC

	M	T	S	P	S	S	S	P		
TGCACAGAGGTCTGGCTGGACCGAGCAGCCTCCTCCTCTAGG	ATG	ACC	TCA	CCC	TCC	AGC	TCT	CCA	8	
GTG	TTC	AGG	TTG	GAG	ACA	TTA	GAT	GGA	24	
AAG	CTG	GAT	TTT	GGG	AGC	GGG	CTG	CCT	CCC	28
AAG	CTG	GAT	TTT	GGG	AGC	GGG	CTG	CCT	CCC	84
K	L	D	F	G	S	G	L	P	P	48
AAG	CTG	GAT	TTT	GGG	AGC	GGG	CTG	CCT	CCC	144
A	A	P	Q	I	R	V	N	L	N	68
AAA	TTC	GCC	CCT	CAG	ATA	AGA	GTC	AAC	CTC	204
P	D	P	N	R	F	D	R	D	R	88
CCG	GAT	CCA	AAC	CGA	TTT	GAC	CGA	GAT	CGG	264
E	D	L	A	G	L	P	E	Y	L	108
GAG	GAT	CTG	GCT	GGG	CTT	CCA	GAG	TAC	CTG	324
E	Y	T	E	G	S	T	G	K	T	128
GAA	TAC	ACA	GAG	GGC	TCC	ACA	GGT	AAG	ACG	384
D	G	V	N	A	C	I	L	P	L	148
GAC	GGA	GTC	AAT	GCC	TGC	ATT	CTG	CCA	CTG	444
Q	P	L	V	N	A	Q	C	T	D	168
CAG	CCC	CTG	GTA	AAT	GCC	CAG	TGC	ACA	GAT	504
I	A	I	E	K	R	S	L	Q	C	188
ATC	GCC	ATT	GAG	AAG	AGG	AGT	CTG	CAG	TGT	564
V	H	A	R	A	C	G	R	F	F	208
GTG	CAT	GCC	CGG	GCC	TGC	GGC	CGC	TTC	TTC	624
G	E	L	P	L	S	L	A	A	C	228
GGT	GAG	CTA	CCC	CTC	TCT	TTG	GCC	GCT	TGC	684
Q	W	D	V	V	S	Y	L			
T	GTG	GAT	GTG	GTA	AGC	TAC	CTC	TTC		

Fig. 2A

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111
Filed: June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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L	E	N	P	H	Q	P	A	S	L	Q	A	T	D	S	Q	G	N	T	V	248
CTG	GAG	AAC	CCA	CAC	CAG	CCC	GCC	AGC	CTG	CAG	GCC	ACT	GAC	TCC	CAG	GGC	AAC	ACA	GTC	744
L	H	A	L	V	M	I	S	D	N	S	A	E	N	I	A	L	V	T	S	268
CTG	CAT	GCC	CTA	GTG	ATG	ATC	TCG	GAC	AAC	TCA	GCT	GAG	AAC	ATT	GCA	CTG	GTG	ACC	ACC	804
M	Y	D	G	L	L	Q	A	G	A	R	L	C	P	T	V	Q	L	E	D	288
ATG	TAT	GAT	GGG	CTC	CTC	CAA	GCT	GGG	GCC	CGC	CTC	TGC	CCT	ACC	GTG	CAG	CTT	GAG	GAC	864
I	R	N	L	Q	D	L	T	P	L	K	L	A	A	K	E	G	K	I	E	308
ATC	GCC	AAC	CTG	CAG	GAT	CTC	ACG	CCT	CTG	AAG	CTG	GCC	AAG	GAG	GGC	AAG	ATC	GAG	924	
I	F	R	H	I	L	Q	R	E	F	S	G	L	S	H	L	S	R	K	F	328
ATT	TTC	AGG	CAC	ATC	CTG	CAG	CGG	GAG	TTT	TCA	GGA	CTG	AGC	CAC	CTT	TCC	CGA	AAG	TTC	984
T	E	W	C	Y	G	P	V	R	V	S	L	Y	D	L	A	S	V	D	S	348
ACC	GAG	TGG	TGC	TAT	GGG	CCT	GTC	CGG	GTG	TCG	CTG	TAT	GAC	CTG	GCT	TCT	GTG	GAC	AGC	1044
C	E	E	N	S	V	L	E	I	I	A	F	H	C	K	S	P	H	R	H	368
TGT	GAG	GAG	AAC	TCA	GTG	CTG	GAG	ATC	ATT	GCC	TTT	CAT	TGC	AAG	AGC	CCG	CAC	CGA	CAC	1104
R	M	V	V	L	E	P	L	N	K	L	L	Q	A	K	W	D	L	L	I	388
CGA	ATG	GTC	GTT	TTG	GAG	CCC	CTG	AAC	AAA	CTG	CTG	CAG	GCG	AAA	TGG	GAT	CTG	CTC	ATC	1164
P	K	F	F	L	N	F	L	C	N	L	I	Y	M	F	I	F	T	A	V	408
CCC	AAG	TTC	TTC	TTA	AAC	TTC	CTG	TGT	AAT	CTG	ATC	TAC	ATG	TTC	ATC	TTC	ACC	GCT	GTT	1224
A	Y	H	Q	P	T	L	K	K	Q	A	A	P	H	L	K	A	E	V	G	428
GCC	TAC	CAT	CAG	CCT	ACC	CTG	AAG	AAG	CAG	GCC	GCC	CCT	CAC	CTG	AAA	GCG	GAG	GTT	GGA	1284
N	S	M	L	L	T	G	H	I	L	I	L	L	G	G	I	Y	L	L	V	448
AAC	TCC	ATG	CTG	CTG	ACG	GGC	CAC	ATC	CTT	ATC	CTG	CTA	GGG	GGG	ATC	TAC	CTC	CTC	GTG	1344
G	Q	L	W	Y	F	W	R	R	H	V	F	I	W	I	S	F	I	D	S	468
GGC	CAG	CTG	TGG	TAC	TTC	TGG	CGG	CGC	CAC	GTG	TTC	ATC	TGG	ATC	TCG	TTC	ATA	GAC	AGC	1404
Y	F	E	I	L	F	L	F	Q	A	L	L	T	V	V	S	Q	V	L	C	488
TAC	TTT	GAA	ATC	CTC	TTC	CTG	TTC	CAG	GCC	CTG	CTC	ACA	GTG	GTG	TCC	CAG	GTG	CTG	TGT	1464
F	L	A	I	E	W	Y	L	P	L	L	V	S	A	L	V	L	G	W	L	508
TTC	CTG	GCC	ATC	GAG	TGG	TAC	CTG	CCC	CTG	CTT	GTG	TCT	GCG	CTG	GTG	GGC	TGG	CTG	1524	
N	L	L	Y	Y	T	R	G	F	Q	H	T	G	I	Y	S	V	M	I	Q	528
AAC	CTG	CTT	TAC	TAT	ACA	CGT	GGC	TTC	CAG	CAC	ACA	GGC	ATC	TAC	AGT	GTC	ATG	ATC	CAG	1584

Fig. 2B

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K V I L R D L L R F L L I Y L V F L F G 548
AAG GTC ATC CTG CGG GAC CTG CTG CGC TTC CTT CTG ATC TAC TTA GTC TTC CTT TTC GGC 1644

F A V A L V S L S Q E A W R P E A P T G 568
TTC GCT GTA GCC CTG GTG AGC CTG AGC CAG GAG GCT TGG CGC CCC GAA GCT CCT ACA GGC 1704

P N A T E S V Q P M E G Q E D E G N G A 588
CCC AAT GCC ACA GAG TCA GTG CAG CCC ATG GAG GGA CAG GAG GAC GAG GGC AAC GGG GCC 1764

Q Y R G I L E A S L E L F K F T I G M G 608
CAG TAC AGG GGT ATC CTG GAA GCC TCC TTG GAG CTC TTC AAA TTC ACC ATC GGC ATG GGC 1824

E L A F Q E Q L H F R G M V L L L L L A 628
GAG CTG GCC TTC CAG GAG CAG CTG CAC TTC CGC GGC ATG GTG CTG CTG CTG CTG CTG GCC 1884

Y V L L T Y I L L L N M L I A L M S E T 648
TAC GTG CTG CTC ACC TAC ATC CTG CTG CTC AAC ATG CTC ATC GCC CTC ATG AGC GAG ACC 1944

V N S V A T D S W S I W K L Q K A I S V 668
GTC AAC AGT GTC GCC ACT GAC AGC TGG AGC ATC TGG AAG CTG CAG AAA GCC ATC TCT GTC 2004

L E M E N G Y W W C R K K Q R A G V M L 688
CTG GAG ATG GAG AAT GGC TAT TGG TGG TGC AGG AAG CAG CGG GCA GGT GTG ATG CTG 2064

T V G T K P D G S P D E R W C F R V E E 708
ACC GTT GGC ACT AAG CCA GAT GGC AGC CCG GAT GAG CGC TGG TGC TTC AGG GTG GAG GAG 2124

V N W A S W E Q T L P T L C E D P S G A 728
GTG AAC TGG GCT TCA TGG GAG CAG ACG CTG CCT ACG CTG TGT GAG GAC CCG TCA GGG GCA 2184

G V P R T L E N P V L A S P P K E D E D 748
GGT GTC CCT CGA ACT CTC GAG AAC CCT GTC CTG GCT TCC CCT CCC AAG GAG GAT GAG GAT 2244

G A S E E N Y V P V Q L L Q S N * 765
GGT GCC TCT GAG GAA AAC TAT GTG CCC GTC CAG CTC CTC CAG TCC AAC TGA 2295

TGGCCCAAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTCCAACCACATCTGCTGGCTCTGGGTCCAGTG
AATTCTGGTGGCAAATATATATTTCACTAACTCAAAAAAAAAAAAAAAAAAAAAAA

Fig. 2C

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Partial human VR2 alternate form

Input file frhob12c4.seg; Output File frhob12c4.tra
 Sequence length 1489

G	R	F	F	Q	K	G	Q	G	T	C	F	Y	F	G	E	L	P	L	19	
GC	GGC	CGC	TTC	TTC	CAG	AAG	GGC	CAA	GGG	ACT	TGC	TTT	TAT	TTC	GGT	GAG	CTA	CCC	CTC	57
S	L	A	A	C	T	K	Q	W	D	V	V	S	Y	L	L	E	N	P	H	39
TCT	TTG	GCC	GCT	TGC	ACC	AAG	CAG	TGG	GAT	GTG	GTA	AGC	TAC	CTC	CTG	GAG	AAC	CCA	CAC	117
Q	P	A	S	L	Q	A	T	D	S	Q	G	N	T	V	L	H	A	L	V	59
CAG	CCC	GCC	AGC	CTG	CAG	GCC	ACT	GAC	TCC	CAG	GGC	AAC	ACA	GTC	CTG	CAT	GCC	CTA	GTG	177
M	I	S	D	N	S	A	E	N	I	A	L	V	T	S	M	Y	D	G	L	79
ATG	ATC	TCG	GAC	AAC	TCA	GCT	GAG	AAC	ATT	GCA	CTG	GTG	ACC	AGC	ATG	TAT	GAT	GGG	CTC	237
L	Q	A	G	A	R	L	C	P	T	V	Q	L	E	D	I	R	N	L	Q	99
CTC	CAA	GCT	GGG	GCC	CGC	CTC	TGC	CCT	ACC	GTG	CAG	CTT	GAG	GAC	ATC	CGC	AAC	CTG	CAG	297
D	L	T	P	L	K	L	A	A	K	E	G	K	I	E	I	F	R	H	I	119
GAT	CTC	ACG	CCT	CTG	AAG	CTG	GCC	GCC	AAG	GAG	GGC	AAG	ATC	GAG	ATT	TTC	AGG	CAC	ATC	357
L	Q	R	E	F	S	G	L	S	H	L	S	R	K	F	T	E	W	C	Y	139
CTG	CAG	CGG	GAG	TTT	TCA	GGA	CTG	AGC	CAC	CTT	TCC	CGA	AAG	TTC	ACC	GAG	TGG	TGC	TAT	417
G	P	V	R	V	S	L	Y	D	L	A	S	V	D	S	C	E	E	N	S	159
GGG	CCT	GTC	CGG	GTG	TCG	CTG	TAT	GAC	CTG	GCT	TCT	GTG	GAC	AGC	TGT	GAG	GAG	AAC	TCA	477
V	L	E	I	I	A	F	H	C	K	S	P	H	R	H	R	M	V	V	L	179
GTG	CTG	GAG	ATC	ATT	GCC	TTT	CAT	TGC	AAG	AGC	CCG	CAC	CGA	CGA	ATG	GTC	GTT	TTG	537	
E	P	L	N	K	L	L	Q	A	K	W	D	L	L	I	P	K	F	F	L	199
GAG	CCC	CTG	AAC	AAA	CTG	CTG	CAG	GCG	AAA	TGG	GAT	CTG	CTC	ATC	CCC	AAG	TTC	TTC	TTA	597
N	F	L	C	N	L	I	Y	M	F	I	F	T	A	V	A	Y	H	Q	P	219
AAC	TTC	CTG	TGT	AAT	CTG	ATC	TAC	ATG	TTC	ATC	TTC	ACC	GCT	GTT	GCC	TAC	CAT	CAG	CCT	657
T	L	K	K	Q	A	A	P	H	L	K	A	E	V	G	N	S	M	L	L	239
ACC	CTG	AAG	AAG	CAG	GCC	GCC	CCT	CAC	CTG	AAA	GCG	GAG	GTT	GGA	AAC	TCC	ATG	CTG	CTG	717
T	G	H	I	L	I	L	L	G	G	I	Y	L	L	V	G	Q	L	W	Y	259
ACG	GGC	CAC	ATC	CTT	ATC	CTG	CTA	GGG	GGG	ATC	TAC	CTC	CTC	GTG	GGC	CAG	CTG	TGG	TAC	777
F	W	R	R	H	V	F	I	W	I	S	F	I	D	S	Y	F	E	I	L	279
TTC	TGG	CGG	CGC	CAC	GTG	TTC	ATC	TGG	ATC	TCG	TTC	ATA	GAC	AGC	TAC	TTT	GAA	ATC	CTC	837

Fig. 3A

Applicant: Rory A. J. Curtis
U.S. Serial No. : 09/587,111
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

Filed: June 2, 2000

9/37

F L F Q A L L T V V S Q V L C F L A I E 299
TTC CTG TTC CAG GCC CTG CTC ACA GTG GTG TCC CAG GTG CTG TGT TTC CTG GCC ATC GAG 897

W Y L P L L V S A L V L G W L N L L Y Y 319
TGG TAC CTG CCC CTG CTT GTG TCT GCG CTG GTG CTG GGC TGG CTG AAC CTG CTT TAC TAT 957

T R G F Q H T G I Y S V M I Q K K A I S 339
ACA CGT GGC TTC CAG CAC ACA GGC ATC TAC AGT GTC ATG ATC CAG AAG AAA GCC ATC TCT 1017

V L E M E N G Y W W C R K K Q R A G V M 359
GTC CTG GAG ATG GAG AAT GGC TAT TGG TGG TGC AGG AAG AAG CAG CGG GCA GGT GTG ATG 1077

L T V G T K P D G S P D E R W C F R V E 379
CTG ACC GTT GGC ACT AAG CCA GAT GGC AGC CCG GAT GAG CCC TGG TGC TTC AGG GTG GAG 1137

E V N W A S W E Q T L P T L C E D P S G 399
GAG GTG AAC TGG GCT TCA TGG GAG CAG ACC CTG CCT ACG CTG TGT GAG GAC CCG TCA GGG 1197

A G V P R T L E N P V L A S P P K E D E 419
GCA GGT GTC CCT CGA ACT CTC GAG AAC CCT GTC CTG GCT TCC CCT CCC AAG GAG GAT GAG 1257

D G A S E E N Y V P V Q L L Q S N * 437
GAT GGT GCC TCT GAG GAA AAC TAT GTG CCC GTC CAG CTC CTC CAG TCC AAC TGA 1311

TGGCCAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTCCAACCACATCTGCTGGCTCTGGGTCCCAGTG

AATTCTGGTGGCAAATATATATTTCACTAACTCAAAAAAAAAAAAAAAAAAAAAAAAAAGGA

GCGGACGCGTGGGTGAC

Fig. 3B

10/37

Partial rat VR2

Input file Flrxrb147g11.seq; Output File Flrxrb147g11.tra
 Sequence length 1794

S	T	H	A	S	A	L	S	L	A	A	C	T	K	Q	W	D	V	V	19		
G	TCG	ACC	CAC	GCG	TCC	GCT	CTT	TCT	CTG	GCT	GCG	TGC	ACC	AAG	CAG	TGG	GAT	GTG	GTG	57	
T	Y	L	L	E	N	P	H	Q	P	A	S	L	E	A	T	D	S	L	G	39	
ACC	TAC	CTC	CTG	GAG	AAC	CCA	CAC	CAG	CCG	GCC	AGC	CTG	GAG	GCC	ACC	GAC	TCC	CTG	GGC	117	
N	T	V	L	H	A	L	V	M	I	A	D	N	S	P	E	N	S	A	L	59	
AAC	ACA	GTC	CTG	CAT	GCT	CTG	GTA	ATG	ATT	GCA	GAT	AAC	TCG	CCT	GAG	AAC	AGT	GCC	CTG	177	
V	I	H	M	Y	D	G	L	L	Q	M	G	A	R	L	C	P	T	V	Q	79	
GTG	ATC	CAC	ATG	TAC	GAC	GGG	CTT	CTA	CAA	ATG	GGG	GCG	CGC	CTC	TGC	CCC	ACT	GTG	CAG	237	
L	E	E	I	S	N	H	Q	G	L	T	P	L	K	L	A	A	K	E	G	99	
CTT	GAG	GAA	ATC	TCC	AAC	CAC	CAA	GGC	CTC	ACA	CCC	CTG	AAA	CTA	GCC	GCC	AAG	GAA	GGC	297	
K	I	E	I	F	R	H	I	L	Q	R	E	F	S	G	P	Y	Q	P	L	119	
AAA	ATC	GAG	ATT	TTC	AGG	CAC	ATT	CTG	CAG	CGG	GAA	TTC	TCA	GGA	CCG	TAC	CAG	CCC	CTT	357	
S	R	K	F	T	E	W	C	Y	G	P	V	R	V	S	L	Y	D	L	S	139	
TCC	CGA	AAG	TTT	ACT	GAG	TGG	TGT	TAC	GGT	CCT	GTG	CGG	GTA	TCG	CTG	TAC	GAC	CTG	TCC	417	
S	V	D	S	W	E	K	N	S	V	L	E	I	I	I	A	F	H	C	K	S	159
TCT	GTG	GAC	AGC	TGG	GAA	AAG	AAC	TCG	GTG	CTG	GAG	ATC	ATC	GCT	TTT	CAT	TGC	AAG	AGC	477	
P	N	R	H	R	M	V	V	L	E	P	L	N	K	L	L	Q	E	K	W	179	
CCG	AAC	CGG	CAC	CGC	ATG	GTG	GTT	TTA	GAA	CCA	CTG	AAC	AAG	CTT	CTG	CAG	GAG	AAA	TGG	537	
D	R	L	V	S	R	P	F	F	N	F	A	C	Y	L	V	Y	M	F	I	199	
GAT	CGG	CTC	GTC	TCA	AGA	TTC	TTC	TTC	AAC	TTC	GCC	TGC	TAC	TTG	GTC	TAC	ATG	TTC	ATC	597	
F	T	V	V	A	Y	H	Q	P	S	L	D	Q	P	A	I	P	S	S	K	219	
TTC	ACC	GTC	GTT	GCC	TAC	CAC	CAG	CCT	TCC	CTG	GAT	CAG	CCA	GCC	ATC	CCC	TCA	TCA	AAA	657	
A	T	F	G	E	S	M	L	L	G	H	I	L	I	L	L	G	G	I	239		
GCG	ACT	TTT	GGG	GAA	TCC	ATG	CTG	CTG	CTG	GGC	CAC	ATT	CTG	ATC	CTG	CTT	GGG	GGT	ATT	717	
Y	L	L	L	G	Q	L	W	Y	F	W	R	R	R	L	F	I	W	I	S	259	
TAC	CTC	TTA	CTG	GGC	CAG	CTG	TGG	TAC	TTT	TGG	CGG	CGG	CGC	CTG	TTT	ATC	TGG	ATC	TCA	777	
F	M	D	S	Y	F	E	I	L	F	L	L	Q	A	L	L	T	V	L	S	279	
TTC	ATG	GAC	AGC	TAC	TTT	GAA	ATC	CTC	TTT	CTC	CTT	CAG	GCT	CTG	CTC	ACA	GTG	CTG	TCC	837	

Fig. 4A

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RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

11/37

Q	V	L	R	F	M	E	T	E	W	Y	L	P	L	L	V	L	S	L	V	299
CAG	GTG	CTG	CGC	TTC	ATG	GAG	ACT	GAA	TGG	TAC	CTA	CCC	CTG	CTA	GTG	TTA	TCC	CTA	GTG	897
L	G	W	L	N	L	L	Y	Y	T	R	G	F	Q	H	T	G	I	Y	S	319
CTG	GGC	TGG	CTG	AAC	CTG	CTT	TAC	TAC	ACA	CGG	GGC	TTT	CAG	CAC	ACA	GGC	ATC	TAC	AGT	957
V	M	I	Q	K	V	I	L	R	D	L	L	R	F	L	L	V	Y	L	V	339
GTC	ATG	ATC	CAG	AAG	GTC	ATC	CTT	CGA	GAC	CTG	CTC	CGT	TTC	CTG	CTG	GTC	TAC	CTG	GTC	1017
F	L	F	G	F	A	V	A	L	V	S	L	S	R	E	A	R	S	P	K	359
TTC	CTT	TTC	GGC	TTT	GCT	GTA	GCC	CTA	GTA	AGC	TTG	AGC	AGA	GAG	GCC	CGA	AGT	CCC	AAA	1077
A	P	E	D	N	N	S	T	V	T	E	Q	P	T	V	G	Q	E	E	E	379
GCC	CCT	GAA	GAT	AAC	AAC	TCC	ACA	GTG	ACG	GAA	CAG	CCC	ACG	GTG	GGC	CAG	GAG	GAG	GAG	1137
P	A	P	Y	R	S	I	L	D	A	S	L	E	L	F	K	F	T	I	G	399
CCA	GCT	CCA	TAT	CGG	AGC	ATT	CTG	GAT	GCC	TCC	CTA	GAG	CTG	TTC	AAG	TTC	ACC	ATT	GGT	1197
M	G	E	L	A	F	Q	E	Q	L	R	F	R	G	V	V	L	L	L	L	419
ATG	GGG	GAG	CTG	GCT	TTC	CAG	GAA	CAG	CTG	CGT	TTT	CGT	GGG	GTG	GTC	CTG	CTG	TTG	CTG	1257
L	A	Y	V	L	L	T	Y	V	L	L	L	N	M	L	I	A	L	M	S	439
TTG	GCC	TAC	GTC	CTT	CTC	ACC	TAC	GTC	CTG	CTG	CTC	AAC	ATG	CTC	ATT	GCT	CTC	ATG	AGC	1317
E	T	V	N	H	V	A	D	N	S	W	S	I	W	K	L	Q	K	A	I	459
GAA	ACT	GTC	AAC	CAC	GTT	GCT	GAC	AAC	AGC	TGG	AGC	ATC	TGG	AAG	TTG	CAG	AAA	GCC	ATC	1377
S	V	L	E	M	E	N	G	Y	W	W	C	R	R	K	K	H	R	E	G	479
TCT	GTC	TTG	GAG	ATG	GAG	AAT	GGT	TAC	TGG	TGG	TGC	CGG	AGG	AAG	AAA	CAT	CGT	GAA	GGG	1437
R	L	L	K	V	G	T	R	G	D	G	T	P	D	E	R	W	C	F	R	499
AGG	CTG	CTG	AAA	GTC	GGC	ACC	AGG	GGG	GAT	GGT	ACC	CCT	GAT	GAG	CGC	TGG	TGC	TTC	AGG	1497
V	E	E	V	N	W	A	A	W	E	K	T	L	P	T	L	S	E	D	P	519
GTG	GAG	GAA	GTA	AAT	TGG	GCT	GCT	TGG	GAG	AAG	ACT	CTT	CCC	ACC	TTA	TCT	GAG	GAT	CCA	1557
S	G	P	G	I	T	G	N	K	K	N	P	T	S	K	P	G	K	N	S	539
TCA	GGG	CCA	GGC	ATC	ACT	GGT	AAT	AAA	AAG	AAC	CCA	ACC	TCT	AAA	CCG	GGG	AAG	AAC	AGT	1617
A	S	E	E	D	H	L	P	L	Q	V	L	Q	S	P	*					555
GCC	TCA	GAG	GAA	GAC	CAT	CTG	CCC	CTT	CAG	GTC	CTC	CAG	TCC	CCC	TGA					1665
TGGCCCGAGATGCAGCAGCAGGCTGGCAGGATGGAGTAGGAACTTCCAGCCACACCAGAGGCTACTGAATTTGGTG																				
GAAATATAATATTTTTTGATXXXXXXXXXXXXAGGGCGGCCGC																				

Fig. 4B

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Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

12/37

GAP of: humanvr2.pep check: 5746 from: 1 to: 764

humanVR2 Flh21e11

to: humanvr1.pep check: 6877 from: 1 to: 839

humanVR1 _Fbh18547pat - fchrb87a6, 3909 bases, 4554 checksum.

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1530 Length: 850
Ratio: 2.003 Gaps: 10

Percent Similarity: 55.378 Percent Identity: 46.348

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

humanvr2.pep x humanvr1.pep

1	MTSPSSSPVF	10
1	MKKWSSTDLGTAADPLQKDTC	PDPPLGD	50
11	RLETLDGGQEDGSEADRGK	LDFGSGLPPMESQ	60
51	GKGDSEEA	FVDCPHEEGELDSCP	99
61	RKGTGASQ	PDPNRFD	110
100	DSVAASSTEKLRLYDRRS	I	149
111	TEGSTGKTCLMKA	VLNLDGVNACILPLLQIDRDSGNP	160
150	KDPETGKTCLL	KAMLNLDGQNTTIP	199
161	YRGHSALHIAIEKRS	LQCVKL	209
200	YKGQTALHIAIERRN	MALVTLL	249

Fig. 5A

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210	ELPLSLAACTKQWDVSYLLENPHQPASLQATDSQGNTVLHALVMISDNS	259
250	ELPLSLAACTNQLGIVKFLLQNSWQTADISARDVGNTVLHALVEADNT	299
260	AENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAKEKGKIEI	309
300	ADNTKFVTSMYNEILMLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIV	349
310	FRHILQREFS..GLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEI	357
350	LAYILQREIQEPECRHLSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEV	399
358	IAF.HCKSPHRHRMVVLEPLNKLLQAKWDLLIPK.FFLNFLCNLIYMFIF	405
400	IAYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIF	449
406	TAVAYHQPTLKKQAAPHLKAEVGNSMLLTGHILILLGGIYLLVGQLWYFW	455
450	TMAAYYRPV..DGLPPFKMEKIGDYFRVTGEILSVLGGVYFFFRCGIQYFL	497
456	RRHVFIIWISFIDSYFEILFLFQALLTVVSQVLCFLAIEWYLPLLV SALVL	505
498	QRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLYFSHLKEYVASMVFSLAL	547
506	GWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGFAVALVS	555
548	GWTNMLYYTRGFQQMGIYAVMIEKMLRDLCRFMFVYIVFLFGFSTAVVT	597
556	LSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLELFKFTI	605
598	LIEDGKNDSLPSESTSHWRGPACRPPD....SSYNSLYSTCLELFKFTI	643
606	GMGELAPQEQLHFRGMVLLLLAYVLLTYIILLLNMLIALMSETVNSVATD	655
644	GMGDLEFTENYDFKAVFIILLLAYVILTYIILLLNMLIALMGETVNKIAQE	693
656	SWSIWKLQKAISVLEMENGYWWC.RKKQRAGVMLTVGTKPDGSPDERWCF	704
694	SKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCF	743
705	RVEEVNWASWEQTLPTLCEDPSGA.GVPRTLENPVLASPPKEDEDGASEE	753
744	RVDEVNWTWNTNVGIINEDPGNCEGVKRTLSFLRSS....RVSGRHWK	789
754	NYVPVQLLQSN.....	764
790	NFALVPLLREASARDROSAQPEEVYLROFGSLKPEDAEVFKSPAASGEK	839

Fig. 5B

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Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

14/37

GAP of: humanvr2.seq check: 8853 from: 1 to: 2809

humanVR2 21e11a, 2809 bases, 8853 checksum.

to: humanvrl.seq check: 4554 from: 1 to: 3909

humanVR1 Fbh18547pat - Import - complete

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 14359 Length: 3934

Ratio: 5.112 Gaps: 15

Percent Similarity: 55.316 Percent Identity: 55.316

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

humanvr2.seq x humanvrl.seq

1 GGCTAGCCTGTCCTGACAGGGGAGAG 26
801 TGTCCACAGTAGTCCCCCTTATCCACGGGTGTCACTTCCATGGGTTCA 850
27 TTAAGCTCCCGTTCTCCACCGTGCCGGCTGCCAGGTGGGCTGAGGGTGA 76
851 GTTATTTGCGGTCAACCACGGTCTGCCAATATTAAATGGAAAATTCTTCA 900
77 CCGAGAGACCAGAACCTGCTTGCTGGAGCTAGTGCTCAGAGCTGGGAG 126
901 AACAGTTCCCAAGTTTCCCTTGTCATTGTTCTGAGCAGTGTGATGAAG 950
127 GGAGGTTCCGCCGCTCCCTGCTGTCAGCGCCGGCAGCCCTCCGGCTT 176
951 AGTCTCTGCCGTGCCATCTGGGATGCAAACCGTCCCTGTGTCCCCCACGT 1000

Fig. 6A

177	CACTTCCTCCGCAGCCCTGCTACTGAGAAGCTCCGGGATCCCAGCAGC	226
1001	CCAGGCCGTAGATGCTCCCCGCCGGTCAGTCACTTAGTCGTAGATCGCC	1050
227	CGCCACGCCCTGGC.....	CTCAGCCTGCGGG 253
1051	CGTCCTGGTATCACAGTGCTTCTGTTAGGTTGCCACACTGGGCCACAGAG	1100
254	GCTCCAGTCAGGCCAACACCGACGCGCAGCTGGGAGGAAG.....	293
1101	GATCCAGCAAGGATGAAGAAATGGAGCAGCACAGACTTGGGACAGCTGC	1150
294ACAGGACCCCTTGACATCTCCATCTGCACAGAGGTCTG 331	.
1151	GGACCCACTCCAAAAGGACACCTGCCAGACCCCCCTGGATGGAGACCCCTA	1200
332	GCTGGACCGAGCAGCCTCCTCCTCTAGGATGACCTCACCCCTCCAGC..T	379
1201	ACTCCAGGCCACCTCCAGCCAAGCCCCAGCTCCCCACGGCCAAGAGCCGC	1250
380	CTCCAGTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCT	429
1251	ACCCGGCTTTGGGAAGGGTGAECTCGGAGGAGGCTTCCCGGTGGATTG	1300
430	GAGGCAGACAGAGGAAAGCTGGATTTGGGAGCGGGCTGCCTCCATGGA	479
1301	CCCCCACGAGGAAGGTGAGTTGGACTCCTGCCGACCATCACAGTCAGCC	1350
480	GTCACAGTCCAGGGCAGGACCGGAAATTGCCCTCAGATAAGAGTCA	529
1351	CTGTTATCACCATCCAGAGGCCAGGAGACGGCCCCACCGGTGCCAGG..C	1398
530	ACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCCGGATCCAAACCGA	579
1399	TGCTGTCCAGGACTCTGCGCCGCCAGCACCGAGAACAGCCCTCAGGCTC	1448
580	TTTGACCGAGATCGGCTCTCAATGCGGTCTCCGGGGTGTCCCCGAGGA	629
1449	TATGATCGCAGGAGTATCTTGAAGCCGTTGCTCAGAATAACTGCCAGGA	1498
630	TCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAGCAAGTACCTCACCG	679
1499	TCTGGAGAGGCCCTGCTGCTTCCCTGCGAGAACAGCAAGAACGCCACAG	1548

Fig. 6B

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680 ACTCGGAATACACAGAGGGCTCCACAGGTAAAGACGTGCCTGATGAAGGCT 729
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1549 ACAACGAGTTCAAAGACCCCTGAGACAGGGAAAGACCTGTCTGCTGAAAGCC 1598
730 GTGCTGAACCTTAAGGACGGAGTCATGCCCTGCATTCTGCCACTGCTGCA 779
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1599 ATGCTCAACCTGCACGGACAGAACACCACATCCCCCTGCTCCTGGA 1648
780 GATCGACAGGGACTCTGGCAATCCTCAGCCCCCTGGTAAATGCCAGTGCA 829
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1649 GATCGCGCGCAAACGGACAGCCTGAAGGAGCTTGTCAACGCCAGCTACA 1698
830 CAGATGACTATTACCGAGGCCACAGCGCTCTGCACATGCCATTGAGAAG 879
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1699 CGGACAGCTACTACAAGGGCCAGACAGCACTGCACATGCCATCGAGAGA 1748
880 AGGAGTCTGCAGTGTGTGAAGCTCCTGGTGGAGAATGGGGCAATGTGCA 929
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1749 CGAACATGCCCTGGTGACCCCTCTGGTGGAGAACGGAGCACGTCCA 1798
930 TGCCCGGGCTGCGGCCGCTTCTTCCAGAACGGCCAAG...GGACTTGCT 976
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1799 GGCTGCGGCCATGGGACTTCTTAAGAAAACCAAGGGCGCTGGAT 1848
977 TTTATTCGGTGAGCTACCCCTCTTTGGCCGTTGCACCAAGCAGTGG 1026
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1849 TCTACTCGGTGAACTGCCCTGTCCCTGGCGCGTGCACCAACCAGCTG 1898
1027 GATGTGGTAAGCTACCTCCTGGAGAACCCACACCAGCCGCCAGCCTGCA 1076
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1899 GGCATCGTGAAGTCCCTGCTGCAGAACTCCTGGCAGACGGCGACATCAG 1948
1077 GCCCACTGACTCCCAGGGCAACACAGTCCTGCATGCCCTAGTGATGATCT 1126
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1949 CGCCAGGGACTCGGTGGCAACACGGTGTGCACGCCCTGGTGGAGGTGG 1998
1127 CGGACAACCTCAGCTGAGAACATTGCACTGGTGACCAGCATGTATGATGGG 1176
||| ||| ||| ||| ||| ||| ||| ||| |||
1999 CCGACAACACGGCCGACAACACGAAGTTGTGACGAGCATGTACAATGAG 2048
1177 CTCCCTCCAAGCTGGGGCCCGCCTCTGCCCTACCGTGCAGCTTGAGGACAT 1226
||| ||| ||| ||| ||| ||| ||| ||| |||
2049 ATTCTGATGCTGGGGCCAAACTGCACCCGACGCTGAAGCTGGAGGAGCT 2098

Fig. 6C

Fig. 6D

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1765 TACTTTGAAATCCTCTTCCAGGCCCTGCTCACAGTGGTGTCCCCA 1814
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2643 TACAGTGAGATGCTTCTTCAGTCACAGTGGTACCTGCCCTGCTGTCTG 2692
||||||| ||||| ||||| ||||| ||||| ||||| |||||
1815 GGTGCTGTGTTCTGCCATCGAGTGGTACCTGCCCTGCTGTCTG 1864
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2693 GGTGCTGTACTTCAGCCACCTCAAGGAGTATGGCTTCCATGGTATTCT 2742
1865 CGCTGGTGCCTGGCTGGCTGAACCTGCTTACTATAACACGTGGCTTCCAG 1914
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2743 CCCTGGCCTGGGCTGGACCAACATGCTCTACTACACCCGGTTTCCAG 2792
1915 CACACAGGCATCTACAGTGTATGATCCAGAAGGTCACTCCTGGGGACCT 1964
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2793 CAGATGGGCATCTATGCCGTATGATAGAGAAGATGATCCTGAGAGACCT 2842
1965 GCTGCGCTTCTTCTGATCTACTTAGTCTTCCCTTCGGCTTCGCTGTAG 2014
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2843 GTGCCGTTTCTATGTTGTCTACATCGTCTTCTGTTGGGTTTCCACAG 2892
2015 CCCTGGTGAGCCTGAGCCAGGAGGCTGGCGCCCCGAAGCTCCTACAGGC 2064
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2893 CGGTGGTGACGCTGATTGAAGACGGAAAGATGACTCCCTGCCGTGAG 2942
2065 CCCAATGCCACAGAGTCAGTGCAGCCATGGAGGGACAGGAGGACGGGG 2114
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2943 TCCA.....CGTCGCACAGGTGGGGGGCTGCCTGCAGGCC 2980
2115 CAACGGGGCCAGTACAGGGTATCCTGGAAGCCTCCGGAGCTTTCA 2164
||||||| ||||| ||||| ||||| ||||| ||||| |||||
2981 CCCCGATACTCCCTACAAACAGCCTGTACTCCACCTGCCCTGGAGCTTTCA 3030
2165 AATTCAACCATCGGCATGGCGAGCTGGCCTTCCAGGAGCAGCTGCACTTC 2214
||||||| ||||| ||||| ||||| ||||| ||||| |||||
3031 AGTTCAACCATCGGCATGGCGACCTGGAGTTCACTGAGAACTATGACTTC 3080
2215 CGCGGCATGGTGCCTGCTGCTGCTGGCCTACGTGCTGCTCACCTACAT 2264
||||||| ||||| ||||| ||||| ||||| ||||| |||||
3081 AAGGCTGTCTTCTACATCCTGCTGCTGGCCTATGTAATTCTCACCTACAT 3130
2265 CCTGCTGCTAACATGCTCATGCCCTCATGAGCGAGACCGTCAACAGTG 2314
||||||| ||||| ||||| ||||| ||||| ||||| |||||
3131 CCTCCTGCTAACATGCTCATGCCCTCATGGGTGAGACTGTCAACAAGA 3180

Fig. 6E

Applicant: Rory A. J. Curtis
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Docket No.: MPI98-093P2RCP3DV1AM

Filed: June 2, 2000

19/37

2315	TCGCCACTGACAGCTGGAGCATCTGGAAAGCTGCAGARAGCCATCTCTGTC	2364
3181	TCGCACAGGAGAGCAAGAACATCTGGAAAGCTGCAGAGAGCCATCACCATC	3230
2365	CTGGAGATGGAGAATGGCTATTGGTGGTGCAGGAAGAAG...CAGCGGGC	2411
3231	CTGGACACGGAGAAGAGCTTCCTTAAGTGCATGAGGAAGGCCTCCGCTC	3280
2412	AGGTGTGATGCTGACCGTTGGCACTAACGCCAGATGGCAGCCGGATGAGC	2461
3281	AGGCAAGCTGCTGCAGGTGGGTACACACCTGATGGCAAGGACGACTACC	3330
2462	GCTGGTGCTTCAGGGTGGAGGGAGGTGAACCTGGGCTTCATGGGAGCAGACG	2511
3331	GGTGGTGCTTCAGGGTGGACGAGGTGAACCTGGACCACCTGGAACACCAAC	3380
2512	CTGCCTACGCTGTGTGAGGACCCG...TCAGGGCAGGTGTCCCTCGAAC	2558
3381	GTGGGCATCATCAACGAAGACCCGGCACTGTGAGGGCGTCAAGCGCAC	3430
2559	TCTCGAGAACCCCTGTCTG....GCTTCCCCCTCCCAAGGAGGATGAGGAT	2604
3431	CCTGAGCTTCTCCCTGGGTCAAGCAGAGTTCAAGGAGACACTGGAAGA	3480
2605	GGTGCCTCTGAGGAAACTATGTGCCCGTCCAGCTCCCTCCAGTCCAATG	2654
3481	ACTTTGCCCTGGTCCCCCTTTAAGAGAGGCAAGTGCCTCGAGATAAGGAG	3530
2655	ATGGCCCAGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTCCA	2704
3531	TCTGCTAGCCCCAGGAAGTTATCTGCGACAGTTTCAGGGTCTCTGAA	3580
2705	ACACACATCTGCTGGCTCTGGGTCCCAGTGAATTCTGGTGGCAAATATAT	2754
3581	GCCA.....GAGGACGCTGAGGTCTCAAGAGTCCTGCCGTTCCGGGA	3625
2755	ATTTTCACTAACTCAAAAAAAAAAAAAAAAAAAAAAAA	2804
3626	GAAGTGAGGACGTCACGCAGACAGCACTGTCAACACTGGCCTTAGGAGA	3675
2805	AAAAA.....	2809
3676	CCCCGTTGCCACGGGGGCTGCTGAGGAACACCAGTGCTCTGTCAGCAG	3725

Fig. 6F

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CLUSTAL W (1.74) multiple sequence alignment

Fig. 7

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

21/37

GAP of: ratvr2.pep check: 9190 from: 1 to: 554

ratVR2 Flrxb147g11

to: humanvr2.pep check: 5746 from: 1 to: 764

humanVR2 Flh21e11

Symbol comparison table: /usr/local/gog_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 2182 Length: 766
Ratio: 3.939 Gaps: 4
Percent Similarity: 81.703 Percent Identity: 79.167

Match display thresholds for the alignment(s) :
| = IDENTITY
: = 2
. = 1

ratvr2.pep x humanvr2.pep

1STHASALSLAACTKQWDVVTVLLENPHQPASLEATDSLGNLTVLH 44
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLH 250

45 ALVMIADNSPENSALVIHMYDGLLQMGARLCPTVQLEEISNHQGLTPLKL 94
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 ALVMISDNAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300

95 AAKEGKIEIFRHILQREFSGPYQPLSRKFTEWCYGPVRVSLYDLSSVDSW 144
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 AAKEGKIEIFRHILQREFSG.LSHLSRKFTEWCYGPVRVSLYDLASVDSC 349

145 EKNSVLEIIIAFHCKSPNRHRMVVLEPLNKLLQEKWDRLVSRPFFNFACYL 194
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
350 EENSVLEIIIAFHCKSPHRHRMVVLEPLNKLLQAKWDLIIPKFFLNFLCNL 399

195 VYMFIFTVVAYHQPSLDQPAIPSSKATFGESMILLGHILILLGGIYLLLG 244
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
400 IYMFIFTAVAYHQPTLKKQAAPHLKAEVGNSMLLTGHILILLGGIYLLVG 449

Fig. 8A

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

22/37

245 QLWYFWRRRLFIWISFMDSYFEILFLLQALLTVLSQVLRFMETEWYLPPLL 294
 ||||| .|||||.||||||| .||||| .||| .||| .: |||||
 450 QLWYFWRRRHFIWISFIDSYFEILFLFQALLTVVSQVLCFLAIEWYLPPLL 499
 .
 295 VLSLVLGWLNLYYTRGFQHTGIYSVMIQKVILRDLLRFLLVYLVFLFGF 344
 | .||||||| .||||||| .||||||| .||||||| .||||||| .:|||||||
 500 VSALVLGWLNLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLFGF 549
 .
 345 AVALVSLSRearSPKAPEDNNSTVTEQPTVGQEEE..PAPYRSILDASLE 392
 ||||| .||| .||| .||| .||| .||| .||| .:||| .||| .||| .:|||
 550 AVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLE 599
 .
 393 LFKFTIGMGEAFQEQLRFRGVVLLLLAYVLLTYVLLNMLIALMSETV 442
 ||||| .||||||| .||||||| .||||||| .||||||| .:||||||| .|||||||
 600 LFKFTIGMGEAFQEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETV 649
 .
 443 NHVADNSWSIWKLQKAISVLEMENGYWWCRRKKHREGRLLKGTRGDGTP 492
 | .||||||| .||||||| .||||||| .||||||| .:||| .||| .:||| .|||.
 650 NSVATDSWSIWKLQKAISVLEMENGYWWC.RKKQRAGVMLTVGTPDGSP 698
 .
 493 DERWCFRVEEVNWAWEKTLPTLSEDPSPGPGITGNKNPT....SKPGKN 538
 ||||| .||||||| .||||||| .||||||| .: .||| .||| ..
 699 DERWCFRVEEVNWASWEQTLPTLCEDPSGAGVPRTLLENPVLASPPKEDED 748
 .
 539 SASEEDHLPQLQLQSP 554
 ||||.:.||.|||
 749 GASEENYVPVQLLQSN 764

Fig. 8B

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

23/37

GAP of: humanvr1.seq check: 4554 from: 1 to: 3909

humanVR1 Fbh18547pat - Import - complete

to: ratvr1.seq check: 7921 from: 1 to: 2847

ratVR1.seq AF029310 in GenBank

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: 0.000

Quality: 22717 Length: 3914
Ratio: 7.979 Gaps: 10
Percent Similarity: 82.125 Percent Identity: 82.125

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

humanvr1 . seq x ratvr1 . seq

1001 CCAGGCCGTAGATGCTCCCGCCGGTCAGTCACTTAGTCGTCAGATGCC 1050

1CAGCTCCAAGGCACTTGCTCC 21

1051 CGTCCTGGTATCACAGTGCTTCTGTTAGGTTGCACACTGGGCCACAGAG 1100

22 ATTTGGGGTGTGCCTGCACCT...AGCTGGTTGCAAATTGGGCCACAGAG 68

1101 GATCCAGCAAGGATGAAAGAAATGGAGCAGCACAGACTTGGGGACAGCTGC 1150

69 GATCTGGAAAGGATGGAACAACGGGCTAGCTTAGACTCAGAGGAGTCTGA 118

1151 GGACCCACTCCAAAAGGACACCTGCCAGACCCCTGGATGGAGACCTA 1200

119 GTCCCCACCCCAAGAGAACTCCTGCCCTGGACCCCTCCAGACAGAGACCTA 168

Fig. 9A

24/37

1201 ACTCCAGGCCACCTCCAGCCAAGCCCCAGCTCCCCACGGCCAAGAGCCGC 1250
169 ACTGCAAGCCACCTCCAGTCAAGCCCCACATCTTCACTACCAGGAGTCGT 218
1251 ACCCGGCTTTGGAGGGTGACTCGGAGGGAGGCTTCCGGTGGATTG 1300
219 ACCCGGCTTTGGAGGGTGACTCGGAGGAGGCCTCTCCCTGGACTG 268
1301 CCCCCACGAGGAAGGTGAGTTGGACTCTGCCCGACCATCACAGTCAGCC 1350
269 CCCTTATGAGGAAGGCAGGCTGGCTTCCTGCCCTATCATCACTGTCAGCT 318
1351 CTGTTATCACCATCCAGAGGCCAGGAGACGGCCCCACCGGTGCCAGGCTG 1400
319 CTGTTCTAACTATCCAGAGGCCTGGGATGGACCTGCCAGTGTCAAGGCCG 368
1401 CTGTCCCAGGACTCTGTCGCCAGCACCGAGAAGACCCCTCAGGCTCTA 1450
369 TCATCCCAGGACTCCGTCTCGCTGG...TGAGAAGCCCCGAGGCTCTA 415
1451 TGATCGCAGGAGTATCTTGAAGCCGTGCTCAGAATAACTGCCAGGATC 1500
416 TGATCGCAGGAGCATCTCGATGCTGTGGCTCAGAGTAACGCCAGGAGC 465
1501 TGGAGAGCCTGCTCTTCCTGCAGAAGAGCAAGAACCTCACAGAC 1550
466 TGGAGAGCCTGCTGCCCTTCCTGCAGAGGAGCAAGAACGCCCTGACTGAC 515
1551 AACGAGTTCAAAGACCCCTGAGACAGGGAAAGACCTGTCTGCTGAAAGCCAT 1600
516 AGCGAGTTCAAAGACCCAGAGACAGGAAAGACCTGTCTGCTAAAAGCCAT 565
1601 GCTCAACCTGCACCGACGGACAGAACACCCATCCCCCTGCTCCTGGAGA 1650
566 GCTCAATCTGCACAATGGGCAGAATGACACCCATCGCTCTGCTCCTGGACG 615
1651 TCGCGCGAACCGGACAGCCTGAAGGGAGCTGTCAACGCCAGCTACACG 1700
616 TTGCCCGGAAGACAGACAGCCTGAAGCAGTTGTCAATGCCAGCTACACA 665
1701 GACAGCTACTACAAGGGCCAGACAGCACTGCACATGCCATCGAGAGACG 1750
666 GACAGCTACTACAAGGGCCAGACAGCACTGCACATTGCCATTGAACGGCG 715

Fig. 9B

25/37

1751 CAACATGGCCCTGGTGACCCCTCTGGTGGAGAACGGAGCAGACGTCCAGG 1800
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
716 GAACATGACGCTGGTGACCCCTCTGGTGGAGAACGGAGCAGATGTCCAGG 765
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1801 CTGCGGCCATGGGACTTCTTAAGAAAACCAAAGGGCGCCTGGATTC 1850
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
766 CTGCGGCTAACGGGACTTCTCAAGAAAACCAAAGGGAGGCCTGGCTTC 815
||||||| ||||||| ||||||| ||||||| |||||||
1851 TACTTCGGTGAACCTGCCCTGTCCCTGGCGCGTGCACCAACCAGCTGGG 1900
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
816 TACTTTGGTGAGCTGCCCTGTCCCTGGCTGCGTGCACCAACCAGCTGGC 865
||||||| ||||||| ||||||| |||||||
1901 CATCGTGAAGTTCTGCTGCAGAACACTCTGGCAGACGGCCGACATCAGCG 1950
||||||| ||||||| ||||||| ||||||| |||||||
866 CATTGTGAAGTTCTGCTGCAGAACACTCTGGCAGCCTGCAGACATCAGCG 915
||||||| |||||||
1951 CCAGGGACTCGGTGGGAAACACCGGTGCTGCACGCCCTGGTGGAGGTGCC 2000
||| ||||| ||||||| ||||||| ||||||| |||||||
916 CCCGGGACTCAGTGGGAAACACCGGTGCTCATGCCCTGGTGGAGGTGCCA 965
|||||||
2001 GACAACACGGCCGACAACACGAAGTTGTGACGAGCATGTACAATGAGAT 2050
||| ||||| ||||||| ||||||| ||||||| |||||||
966 GATAACACAGTTGACAACACCAAGTCGTGACAAGCATGTACAACGAGAT 1015
|||||||
2051 TCTGATGCTGGGGCCAAACTGCACCCGACGCTGAAGCTGGAGGAGCTCA 2100
||||||| ||||||| ||||||| ||||||| |||||||
1016 CTTGATCCTGGGGCCAAACTCCACCCACGCTGAAGCTGGAAGAGATCA 1065
|||||||
2101 CCAACAAGAAGGAATGACGCCGCTGGCTCTGGCAGCTGGACCGGGAAAG 2150
||| ||||| ||||||| ||||||| |||||||
1066 CCAACAGGAAGGGCTCACGCCACTGGCTCTGGCTGCTAGCAGTGGGAAG 1115
|||||||
2151 ATCGGGGTCTGGCCTATATTCTCCAGCGGGAGATCCAGGAGCCCGAGTG 2200
||||||| ||||||| ||||||| |||||||
1116 ATCGGGGTCTGGCCTACATTCTCCAGAGGGAGATCCATGAACCCGAGTG 1165
|||||||
2201 CAGGCACCTGTCCAGGAAGTTACCCGAGTGGGCCTACGGGCCGTGCACT 2250
||| ||||| ||||||| ||||||| |||||||
1166 CCGACACCTATCCAGGAAGTCACCGAATGGCCTATGGCCAGTGCACCT 1215
|||||||
2251 CCTCGCTGTACGACCTGTCCCTGCATCGACACCTGCGAGAAGAACTCGGTG 2300
||||||| ||||||| ||||||| |||||||
1216 CCTCCCTTATGACCTGTCCCTGCATTGACACCTGTGAAAAGAACTCGGT 1265

Fig. 9C

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

26/37

2301 CTGGAGGTGATCGCCTACAGCAGCAGCGAGACCCCTAACGCCACGACAT 2350
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1266 CTGGAGGTGATCGCTTACAGCAGCAGTGAGACCCCTAACCGTCATGACAT 1315
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2351 GCTCTTGGTGAGCCGCTGAACCGACTCCTGCAGGACAAGTGGGACAGAT 2400
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1316 GCTTCTCGTGGAACCCCTGAACCGACTCCTACAGGACAAGTGGGACAGAT 1365
||||| ||||| ||||| ||||| ||||| ||||| |||||
2401 TCGTCAAGCGCATCTTCTACTTCAACTTCCCTGGTCTACTGCCCTGTACATG 2450
||||||| ||||| ||||| ||||| ||||| ||||| |||||
1366 TTGTCAAGCGCATCTTCTACTTCAACTTCCGTCTACTGCTTGTATATG 1415
||||| ||||| ||||| ||||| ||||| ||||| |||||
2451 ATCATCTTCACCATGGCTGCCTACTACAGGCCCGTGGATGGCTTGCCCTCC 2500
||||||| ||||| ||||| ||||| ||||| ||||| |||||
1416 ATCATCTTCACCGCGGCTGCCTACTATCGGCCTGTGGAAAGGCTTGCCCCC 1465
||||| ||||| ||||| ||||| ||||| ||||| |||||
2501 CTTTAAGATGAAAAAA...TTGGAGACTATTCCGAGTTACTGGAGAGA 2547
||||| ||||| ||||| ||||| ||||| ||||| |||||
1466 CTATAAGCTGAAAAAACCCGTTGGGACTATTCCGAGTCACCGGAGAGA 1515
||||| ||||| ||||| ||||| ||||| ||||| |||||
2548 TCCTGTCTGTGTTAGGAGGAGTCTACTTCTTTTCCGAGGGATTCACTAT 2597
||||| ||||| ||||| ||||| ||||| ||||| |||||
1516 TCTTGTCTGTGTCAGGAGGAGTCTACTTCTTCCGAGGGATTCAATAT 1565
||||| ||||| ||||| ||||| ||||| ||||| |||||
2598 TTCCCTGCAGAGGCGGCCGTCGATGAAGACCCCTGTTGTGGACAGCTACAG 2647
||||||| ||||| ||||| ||||| ||||| ||||| |||||
1566 TTCCCTGCAGAGGCGACCATCCCTCAAGAGTTGTTGTGGACAGCTACAG 1615
||||| ||||| ||||| ||||| ||||| ||||| |||||
2648 TGAGATGCTTTCTTCTGCAGTCACTGTTCATGCTGGCCACCGTGTTGC 2697
||||| ||||| ||||| ||||| ||||| ||||| |||||
1616 TGAGATACTTTCTTGTACAGTCGCTGTTCATGCTGGTGTCTGTGGTAC 1665
||||| ||||| ||||| ||||| ||||| ||||| |||||
2698 TGTACTTCAGCCACCTCAAGGAGTATGTGGCTTCCATGGTATTCTCCCTG 2747
||||| ||||| ||||| ||||| ||||| ||||| |||||
1666 TGTACTTCAGCCAACGCAAGGAGTATGTGGCTTCCATGGTGTCTCCCTG 1715
||||| ||||| ||||| ||||| ||||| ||||| |||||
2748 GCCTTGGCTGGACCAACATGCTCTACTACACCCCGGGTTCCAGCAGAT 2797
||||| ||||| ||||| ||||| ||||| ||||| |||||
1716 GCCATGGGCTGGACCAACATGCTCTACTATACCCGAGGATTCCAGCAGAT 1765
||||| ||||| ||||| ||||| ||||| ||||| |||||
2798 GGGCATCTATGCCGTATGATAGAGAAGATGATCCTGAGAGACCTGTGCC 2847
||||| ||||| ||||| ||||| ||||| ||||| |||||
1766 GGGCATCTATGCTGTATGATTGAGAAGATGATCCTCAGAGACCTGTGCC 1815
||||| ||||| ||||| ||||| ||||| ||||| |||||

Fig. 9D

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

27/37

2848 GTTCATGTTGTCTACATCGTCTTGTTCGGGTTTCCACAGCGGTG 2897
1816 GTTTATGTCGTCTACCTCGTCTTGGATTTCCACAGCTGTG 1865

2898 GTGACGCTGATTGAAGACGGGAAGAATGACTCCCTGCCGTCTGAGTCCAC 2947
1866 GTGACACTGATTGAGGATGGGAAGAATAACTCTGCCTATGGAGTCCAC 1915

2948 GTGCACAGGTGGCGGGGCCTGCCTGCAGGCCCGATAGCTCCTACA 2997
1916 ACCACACAAGTGCCGGGGTCTGCCTGCAAG...CCAGGTAACTCTTACA 1962

2998 ACAGCCTGTACTCCACCTGCCTGGAGCTGTTCAAGTCACCATGGCATG 3047
1963 ACAGCCTGTATTCCACATGCTGGAGCTGTTCAAGTCACCATGGCATG 2012

3048 GGCACCTGGAGTTCACTGAGAACTATGACTTCAGGCTGTCTTCATCAT 3097
2013 GGCACCTGGAGTTCACTGAGAACTACGACTTCAGGCTGTCTTCATCAT 2062

3098 CCTGCTGCTGCCATGTAAATTCTCACCTACATCCTGCTAACATGC 3147
2063 CCTGTTACTGCCATGTGATTCTCACCTACATCCTGCTAACATGC 2112

3148 TCATGCCCTCATGGGTGAGACTGTCAACAAGATCGCACAGGAGAGCAAG 3197
2113 TCATTGCTCTCATGGGTGAGACCGTCAACAAGATTGCACAAGAGAGCAAG 2162

3198 AACATCTGGAAGCTGCAGAGAGCCATCACCATCCTGGACACGGAGAGAG 3247
2163 AACATCTGGAAGCTGCAGAGAGCCATCACCATCCTGGATACAGAGAGAG 2212

3248 CTTCTTAAAGTCATGAGGAAGGCCTTCCGTCAGGCAAGCTGCTGCAGG 3297
2213 CTTCTGAAGTCATGAGGAAGGCCTTCCGCTCTGGCAAGCTGCTGCAGG 2262

3298 TGGGGTACACACCTGATGCAAGGACGACTACCGGTGGTGCTTCAGGGTG 3347
2263 TGGGGTTCACTCCTGACGGCAAGGATGACTACCGGTGGTGTTCAGGGTG 2312

3348 GACGAGGTGAACGGACCACTGGAACACCAACCAACGTGGCATCATCAACGA 3397
2313 GACGAGGTAAACTGGACTACCTGGAACACCAACCAATGTGGGTATCATCAACGA 2362

Fig. 9E

28/37

3398 AGACCCGGGCAACTGTGAGGGCGTCAAGCGCACCCCTGAGCTTCTCCCTGC 3447
2363 GGACCCAGGCAACTGTGAGGGCGTCAAGCGCACCCCTGAGCTTCTCCCTGA 2412
3448 GGTCAAGCAGAGTTTCAGGCAGACACTGGAAGAACTTTGCCCTGGTCCC 3497
2413 GGTCAAGCAGAGTTTCAGGGAGAAACTGGAAGAACTTTGCCCTGGTCCC 2462
3498 CTTTTAAGAGAGGCAAGTGCCTCGAGATAGGCAGTCTGCTCAGCCCGAGGA 3547
2463 CTTCTGAGGGATGCAAGCACTCGAGATAGACATGCCACCCAGCAGGAAGA 2512
3548 AGTTTATCTGCGACAGTTTCAGGGCTCTGAAGCCAGAGGACGCTGAGG 3597
2513 AGTTCAACTGAAGCATTATACGGGATCCCTTAAGCCAGAGGATGCTGAGG 2562
3598 TCTTCAAGAGTCCTGCCGCTTCCGGGGAGAAAGTGA.GGACGTCACGCAGA 3646
2563 TTTTCAAGGATTCCATGGTCCCAGGGGAGAAATAATGGACACTATGCAGG 2612
3647 CAGCACTGTCAACACTGGCCTTAGGAGACCCGTTGCCACGGGGGGCTG 3696
2613 GATCAATG.....CGGGGTCTTGGGTGGTCTG 2640
3697 CTGAGGGAACACCAGTGCCTGTCAGCAGCCTGGCTGGTCTGTGCCCTGC 3746
2641 CTTAGGGAAC.CAGCAGGGTTGACGTTATCTGGTCCACTCTGTGCCCTGC 2689
3747 CCA.GCATGTTCCAAATCTGTGCTGGACAAGCTGTGGGAAGCGTTCTTG 3795
2690 CTAGGCACATTCTAGGACTTCGGCGGGCTGCTGTGGGAA.CTGGGAGG 2738
3796 GAAGCATGGGAGTGTACATCCAACCGTCACTGTCCCCAAGTGAATC 3845
2739 TGTGTGGGAATTGAGATGTGTATCCAACCATGA...TCTCCAAACATTG 2785
3846 TCCTAACAGACTTTCAGGTTTTACTCACTTTACTAAAAAAAAAAAAAA 3895
2786 GCTTTCAACTTTATGGACTTTATTAAACAGAGTGAATGGCAAATCTCT 2835
3896 AGGGCGGGCCGCTTA 3909
2836 ACTTGGACACAT.. 2847

Fig. 9F

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

29/37

GAP of: humanvr1.pep check: 6877 from: 1 to: 839

humanVR1_Fbh18547pat - fchrb87a6, 3909 bases, 4554 checksum.

to: ratvr1.pep check: 5764 from: 1 to: 838

ratVR1 | AF029310 Rattus norvegicus vanilloid receptor subtype 1 mRNA, complete cds.

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompoCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 3734 Length: 840
Ratio: 4.456 Gaps: 3

Percent Similarity: 89.247 Percent Identity: 86.022

Match display thresholds for the alignment(s):

IDENTITY

— i = 2

1

humanvr1.pep x ratvr1.pep

51 GKGDSEEA~~FPVDCPHEEGELDSCP~~TI~~VSPVITI~~Q~~RPGDGT~~GA~~RLSQD~~ 100
||||||| .|||:||| | ||| | ||| |:||| ||||| | | |||
51 GKGDSEEA~~SPLD~~CPY~~EEGLASC~~PI~~ITVSSL~~T~~IORPGDGP~~AS~~VPRPSSQD~~ 100

101 SVAASTEKTLLYDRRSIFEAVAQNNCQDLESLLLFLQSKSKHLTDNEFK 150
||.|| || |||||:|||.:|||:|||:||| ||| .|||
101 SVSAG.EKPPRLYDRRSIFDAVAQSNCQELESLLPFLQRSKRLTDSEFK 149

201 KGQTALHIAIERRNMALVTLLVENGADVQAAAHDFFKKTGGRPGFYFGE 250
||||| ||||| ||||| ||||| ||||| . ||||| ||||| |||||
200 KGQTALHIAIERRNMTLVTLVENGADVQAAANGDFFKKTGGRPGFYFGE 249

Fig. 10A

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 Filed: June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

30/37

251 LPLSLAACTNQLGIVKFLLQNSWQTADISARDSVGNTVLHALVEADNTA 300
||||| ||||| ||||| ||||| ||||| ||||| |||||
250 LPLSLAACTNQLAIVKFLLQNSWQPADISARDSVGNTVLHALVEADNTV 299
||||| ||||| . ||||| . : ||| : ||| . |||||
301 DNTKFVTSMYNEILMLGAKLHPTLKLEELTNKKGMTPLALAAGTGKIGVL 350
||||| ||||| . ||||| . : ||| : ||| . |||||
300 DNTKFVTSMYNEILILGAKLHPTLKLEEITNRKGLTPLALAASSGKIGVL 349
||||| ||||| . ||||| . : ||| : ||| . |||||
351 AYILQREIQEPECRHLRSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVI 400
||||| ||||| . ||||| . : ||| : ||| . |||||
350 AYILQREIHEPECRHLRSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVI 399
||||| ||||| . ||||| . : ||| : ||| . |||||
401 AYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFT 450
||||| ||||| . ||||| . : ||| : ||| . |||||
400 AYSSSETPNRHDMLLVEPLNRLLQDKWDRFVKRIFYFNFFVYCLYMIIFT 449
||||| ||||| . ||||| . : ||| : ||| . |||||
451 MAAYYRPVDGLPPFKMEK. IGDYFRVTGEILSVLGGVYFFFTRGIQYFLQR 499
||||| : ||||| : . : ||||| : ||||| . |||||
450 AAAYYRPVEGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFFTRGIQYFLQR 499
||||| : ||||| : . : ||||| : ||||| . |||||
500 RPSMKTLFVDSYSEMLFFLQSLFMLATVVLYFSHLKEYVASMVFSLALGW 549
||||| : . ||||| . . ||||| . . ||||| . : |||
500 RPSLKSLFVDSYSEILFFVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGW 549
||||| : . ||||| . . ||||| . . ||||| . : |||
550 TNMLYYTRGFQQMGIYAVMIEKMLRDLCRFMFVYIVFLFGFSTAVVTLI 599
||||| : . ||||| . . ||||| . . ||||| . : |||||
550 TNMLYYTRGFQQMGIYAVMIEKMLRDLCRFMFVYLVFLFGFSTAVVTLI 599
||||| : . ||||| . . ||||| . . ||||| . : |||||
600 EDGKNDSLPSESTSHWRGPAACRPPDSSNSLYSTCLELFKFTIGMGDLE 649
||||| : . ||||| : . ||||| : . ||||| . . |||||
600 EDGKNNSLPMESTPHKCRGSACK. PGNSNSLYSTCLELFKFTIGMGDLE 648
||||| : . ||||| : . ||||| : . ||||| . . |||||
650 FTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNKIAQESKNIWK 699
||||| : . ||||| : . ||||| : . ||||| . . |||||
649 FTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNKIAQESKNIWK 698
||||| : . ||||| : . ||||| : . ||||| . . |||||
700 LQRAITILDTEKSLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVN 749
||||| : . ||||| : . ||||| : . ||||| . . |||||
699 LQRAITILDTEKSLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVDEVN 748
||||| : . ||||| : . ||||| : . ||||| . . |||||
750 WTTWNTNVGIINEDPGNCEGVKRTLSFSLRSSRVSGRHWNKFALVPLLRE 799
||||| : . ||||| : . ||||| : . ||||| . . |||||
749 WTTWNTNVGIINEDPGNCEGVKRTLSFSLSGRVSGRNWNKFALVPLLKD 798
||||| : . ||||| : . ||||| : . ||||| . . |||||
800 ASARDRQSAQPEEVYLQRQFSGSLKPEDAEVFKSPAASGEK 839
||||| : . ||||| : . ||||| : . ||||| . . |||||
799 ASTRDRHATQQEEVQLKHYTGSLKPEDAEVFKDSMVPGEK 838
||||| : . ||||| : . ||||| : . ||||| . . |||||

Fig. 10B

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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CLUSTAL W (1.74) multiple sequence alignment

humanVR2.alt	-----
human VR2	MTSPSSSPVFRILETLGGQEDGSEADRGKLDGSGLPPMESQFQGEDRKFAPQIRVNLNY
humanVR2.alt	-----
human VR2	RKGTGASQPDPNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL
humanVR2.alt	-----
human VR2	MKAVLNLDGVNACILPLIQLIDRDSGNPQLVNAQCTDDYYRGHSALHIAIEKRSLQCVK
humanVR2.alt	-----
human VR2	GRFFQKGQGTCFYFGEPLSLAACTKQWDVSYLLENPHQPASLQA LLVENGANVHARACGRFFQKGQGTCFYFGEPLSLAACTKQWDVSYLLENPHQPASLQA *****
humanVR2.alt	-----
human VR2	TDSQGNTVLHALVMISDNASENIALVTSMYDGLIQAGARLCPTVQLEDIRNLQDLTPLKL TDSQGNTVLHALVMISDNASENIALVTSMYDGLIQAGARLCPTVQLEDIRNLQDLTPLKL *****
humanVR2.alt	-----
human VR2	AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIIAF AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIIAF *****
humanVR2.alt	-----
human VR2	HCKSPHRHRMVVLEPLNKLQQAKWDLIIPKFFDNFLCNLIYMFIFTAVAYHQPTLKKQAA HCKSPHRHRMVVLEPLNKLQQAKWDLIIPKFFDNFLCNLIYMFIFTAVAYHQPTLKKQAA *****
humanVR2.alt	-----
human VR2	PHLKAEVGNSMILLTGHILILLGGIYLGVQLWYFWRRHVFIIWISFIDSYFEILFLFQALL PHLKAEVGNSMILLTGHILILLGGIYLGVQLWYFWRRHVFIIWISFIDSYFEILFLFQALL *****
humanVR2.alt	-----
human VR2	TVVSQVLCFLAIIEWYLPPLLVSALVLGWLNLYYTRGFQHTGIYSVMIQ----- TVVSQVLCFLAIIEWYLPPLLVSALVLGWLNLYYTRGFQHTGIYSVMIQKVILRDLLRFLL *****
humanVR2.alt	-----
human VR2	IYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLEL *****
humanVR2.alt	-----
human VR2	FKFTIGMGEAFQEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW *****
humanVR2.alt	-----
human VR2	--KKAISVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWASWEQTLPT KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWASWEQTLPT *****
humanVR2.alt	-----
human VR2	LCEDPSGAGVPRTLLENPVLASPPKEDEDGASEENYVPVQLQSN LCEDPSGAGVPRTLLENPVLASPPKEDEDGASEENYVPVQLQSN *****

Fig. 11

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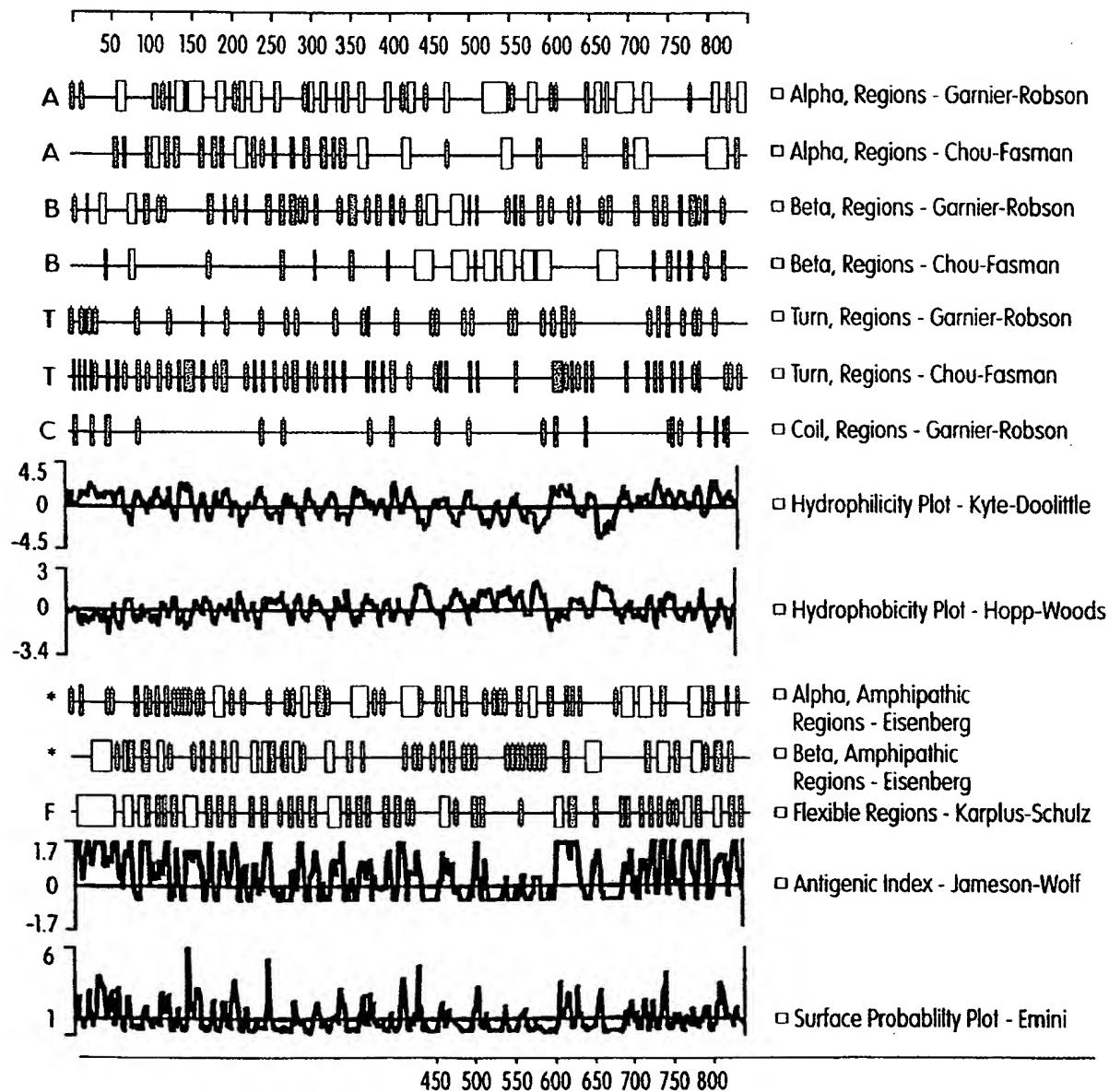


Fig. 12

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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Protein Family / Domain Matches, HMMer version 2

Searching for complete domains

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.2/Pfam

Sequence file: /usr/ns-home/docs/seqanal/orfanal/oa-script 18670 seq

Query: hVR-1

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	Ank repeat	51.5	1.9e-11	3

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/3	201	233	..	1	33 []	34.4 2.6e-06
ank	2/3	248	283	..	1	33 []	13.2 2
ank	3/3	333	361	..	1	33 []	3.4 26

Alignments of top-scoring domains:

ank: domain 1 of 3, from 201 to 233: score 34.4, E = 2.6e-06

->nGnTPLH1Aarygnvevvk1LLehGAdvnartk<-

+G+T+LH+A + n+ +v 1L+e+GAdv a+

hVR-1 201 KGQTALHIAIERRNMALVTLLVENGADVQAAH 233

ank: domain 2 of 3, from 248 to 283: score 13.2, E = 2

->nGnTPLH1Aarygnvevvk1LLe...hGAdvnartk<-

G PL 1Aa +++ +vk+LL+++ + Ad+ ar+

hVR-1 248 FGELPLSLAACTNQLGIVKFLLQnswQTADISARDS 283

ank: domain 3 of 3, from 333 to 361: score 3.4, E = 26

->nGnTPLH1Aarygnvevvk1LLehGAdvnartk<-

+G TPL 1Aa +g++ v ++ L+ +

hVR-1 333 KGMTPLALAAAGTGKIGVLAYILQ---REIQEP 361

Fig. 13

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
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 RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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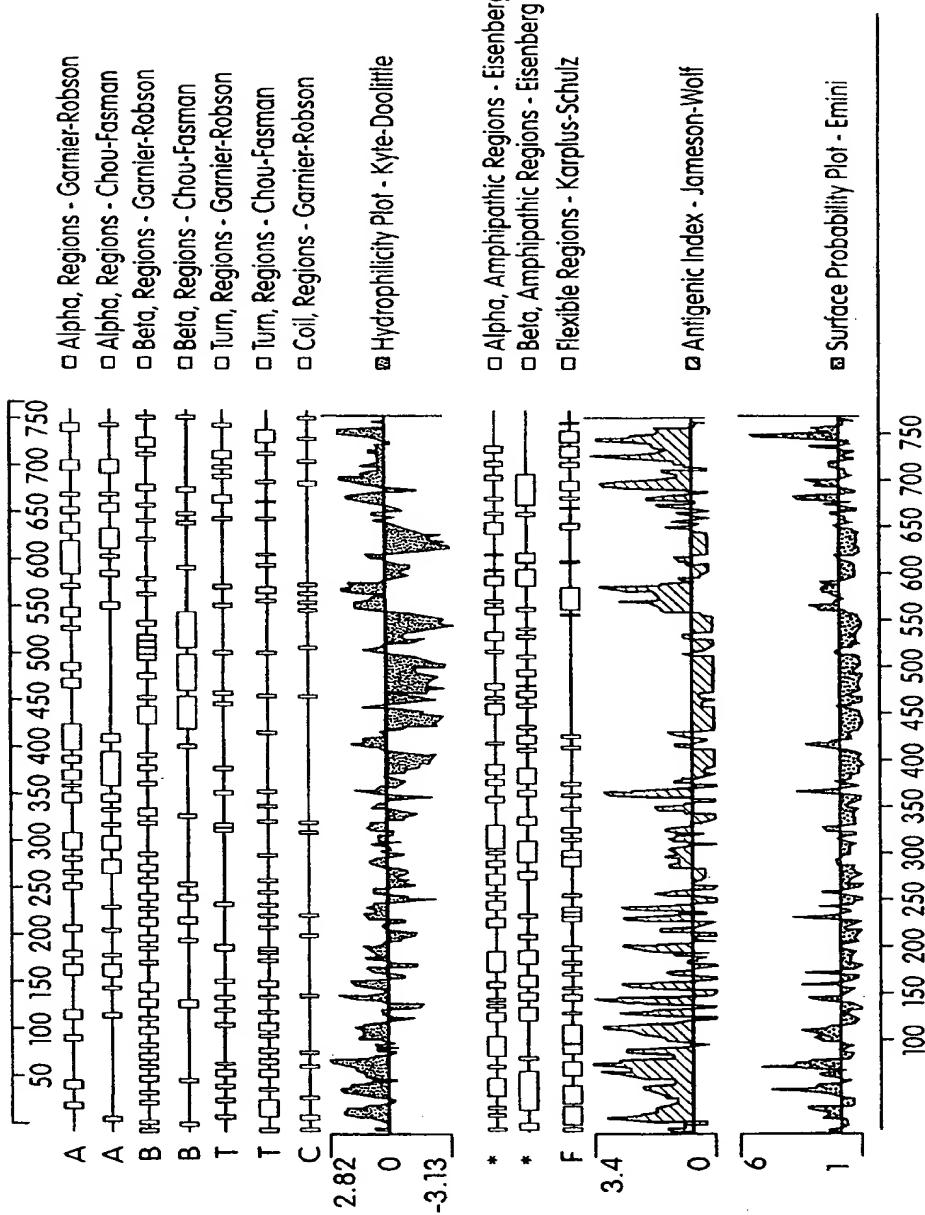


Fig. 14

Applicant: Rory A. J. Curtis
U.S. Serial No. : 09/587,111 Filed: June 2, 2000
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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Protein Family / Domain Matches, HMMer version 2

Searching for complete domains

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.2/Pfam

Sequence file: /tmp/orfanal.5/g.aa

Query: Flh21e11

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
ank	PF00023 Ank repeat	53.7	4e-12	3

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
ank	1/3	162	194	..	1	33 []	38.3 1.7e-07
ank	2/3	208	243	..	1	33 []	6.4 4.3
ank	3/3	293	328	..	1	33 []	8.8 2.1

Alignments of top-scoring domains:

ank: domain 1 of 3, from 162 to 194: score 38.3, E = 1.7e-07

->nGnTPLHlAarygnvevvkllLehGAdvnartk<-

+G+++LH+A ++ ++++vkllL+e+GA+v+ar

Flh21e11 162 RGHSALHIAIEKRSIQCVKLLVENGANVHARAC 194

ank: domain 2 of 3, from 208 to 243: score 6.4, E = 4.3

->nGnTPLHlAarygnvavvkllLe...hGAdvnartk<-

G PL lAa + +++vv +LLe++++ A+ a++

Flh21e11 208 FGELPLSLAACTKQWDVVSYGLEnphQPASLQATDS 243

ank: domain 3 of 3, from 293 to 328: score 8.8, E = 2.1

->nGnTPLHlAarygnvevvkllLe...hGAdvnart<-

+ +TPL lAa++g++e+ + L+++ G + +r

Flh21e11 293 QDLTPLKLAKEQKLEIFRHILQrafSGLSHLSRK 328

Fig. 15

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111
Title: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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>hvr2.alnfl (full-length predicted)
MTSPSSSPVFRLETLDGGQEDGSEADRGLDKLDFGSGLPPMESQFQGEDRKFAPQIRVNLLNY
RKGTGASQPDPPNRFDRDRLFNAVRGVPEDLAGLPEYLSTSKYLTDSSEYTEGSGTGTCL
MKAVLNLKDGVNACILPLQIDRDSGNPQLPVNAQCTDDYRGHSALHIAIEKRSLQCVK
LLVENGANVHARACGRFFQKGQGTFCYFGELPLSLAACTKQWDVVSYLENPHQPAQLQATSQGNTVLHALVM
ISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAREGKIEIFRHIL
QREFSGGLSHLSRKFTEWCYGPVRSVLYDLASVDSCEENSVLEIIFHCKSPHRHMVVL
PLNKLLQAKWDLILPKFFNFLCNLILYMFIFTAVAYHQPTLKKQAAAPHLKAEVGNSMLLT
GHILILGGIYLLVGQLWYWFRRHVFIIWISFIDSYFEILFLQALLTVVSQVLCLFLATEW
YLPLLLVSALVLGWLNLLYTRGFQHTGIYSVMIQKKAISVULEMENGYWWCRKKQRAGVML
TVGTKPDGSPDERWCFRVEEVNWAWEQTLPTLCEDPSGAGVPRTLLENPVLASPPKEDD
GASEENXVVPVQLLQSN

Fig. 16

Applicant: Rory A. J. Curtis
U.S. Serial No.: 09/587,111 **Filed:** June 2, 2000
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RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
Agent: Mario Cloutier
Docket No.: MPI98-093P2RCP3DV1AM

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CLUSTAL W (1.74) multiple sequence alignment

humanVR2	MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGLPPMESQFQGEDRKFAPQIRVNLNY
hVR2.altFL	MTSPSSSPVFRLETLDGGQEDGSEADRGKLDGSGLPPMESQFQGEDRKFAPQIRVNLNY *****
humanVR2	RKGTGASQPDPNRFDRLFNAVRGVPEDLAGLPEYLSKTSKYLTDTSEYTEGSTGKTC
hVR2.altFL	RKGTGASQPDPNRFDRLFNAVRGVPEDLAGLPEYLSKTSKYLTDTSEYTEGSTGKTC *****
humanVR2	MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK
hVR2.altFL	MKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLQCVK *****
humanVR2	LLVENGANVHARACGRFFQKGQGTCFYFELPLSAACTKQWDVVSYLLLENPHQPASLQA
hVR2.altFL	LLVENGANVHARACGRFFQKGQGTCFYFELPLSAACTKQWDVVSYLLLENPHQPASLQA *****
humanVR2	TDSQGNTVLHALVMISDNAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL
hVR2.altFL	TDSQGNTVLHALVMISDNAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL *****
humanVR2	AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF
hVR2.altFL	AAKEGKIEIFRHILQREFSGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF *****
humanVR2	HCKSPHRHRMVVLEPLNKLQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAA
hVR2.altFL	HCKSPHRHRMVVLEPLNKLQAKWDLLIPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAA *****
humanVR2	PHLKAEVGNSMLLTGHILILLGGIYLLVGQLWYFWRHVFIWISFIDSYFEILFLFQALL
hVR2.altFL	PHLKAEVGNSMLLTGHILILLGGIYLLVGQLWYFWRHVFIWISFIDSYFEILFLFQALL *****
humanVR2	TVVSQVLCFLAIEWYLPPLLVSALVLGWLNLYYTRGFQHTGIYSVMIQKVLIRDLLRFL
hVR2.altFL	TVVSQVLCFLAIEWYLPPLLVSALVLGWLNLYYTRGFQHTGIYSVMIQK----- *****
humanVR2	IYLVFLFGFAVALVSLSQEAWRPEAPTGPATESVQPMEGQEDEGNGAQYRGILEASLE
hVR2.altFL	-----
humanVR2	FKFTIGMGECAFQEQLHFRGMVLLAYVLLTYILLLNLIALMSETVNSVATDSWSI
hVR2.altFL	-----
humanVR2	KLQKAISVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWASWEQTLPT
hVR2.altFL	---KAISVLEMENGYWWCRKKQRAGVMLTVGTPDGSPDERWCFRVEEVNWASWEQTLPT *****
humanVR2	LCEDPSGAGVPRLENPVLASPPKEDEDGASEEENYVPVQLLQSN
hVR2.altFL	LCEDPSGAGVPRLENPVLASPPKEDEDGASEEENYVPVQLLQSN *****

Fig. 17